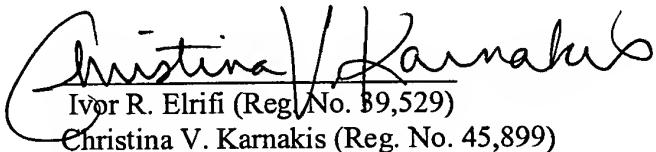


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compliance with 37 C.F.R. §§ 1.821-1.825. The specification has been amended to correct typographical errors, to insert SEQ ID NOs and to insert the sequence listing.

The Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 21402-225 (Cura-525). Should any questions or issues arise concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,



September 17, 2002

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Table 1E was amended as follows:

Table 1E. Domain Analysis of NOV1

gnl|Smart|smart00042, CUB, Domain first found in C1r, C1s, uEGF, and bone morphogenetic protein; This domain is found mostly among developmentally-regulated proteins. Spermadhesins contain only this domain.

CD-Length = 114 residues, 99.1% aligned

Score = 85.5 bits (210), Expect = 1e-17

Query:	799	CGGELGDYTYIESPNYPGDYPANAECVWHIAPPPKRRIILIVVPEIFLPIEDECG-DVLV	857
		CGG L +G I SPNYP YP N CVW I+ PP RI + + L D C D +	
Sbjct:	1	CGGTLTASSGTITS PNPNSYPNNLNCVWTISAPPGYRIELKFTDFDLESSDNCTYDYVE	60
Query:	858	MRKSASPTSITTYETCQTYERPIAFTSRSRKLWIQFKSNEGNSGKGFQVPYVT	910
		+ S +S C + P +S S + + F S+ +GF Y	
Sbjct:	61	IYDGPSTSSPLLGRFCGSELPPPIISSSSNSMTVTFVSDSSVQKRGFSARYSA	113 <u>(SEQ</u>
		<u>ID NO: 181)</u>	

Table 2K on page 35 was amended as follows:

Table 2K. Domain Analysis of NOV2

gnl|Smart|smart00110, C1Q, Complement component C1q domain.; Globular domain found in many collagens and eponymously in complement C1q. When part of full length proteins these domains form a 'bouquet' due to the multimerization of heterotrimers. The C1q fold is similar to that of tumour necrosis factor.

CD-Length = 132 residues, 84.1% aligned
Score = 86.7 bits (213), Expect = 1e-18

Query: 91	MAVTFDKVYVNIGGDFAAAGVFRCLPGAYFFSFTLGKLPRTLSVKLMKNRDEVQAMI
150	V FDKV N G +D + G F C +PG Y+FS+ + + + + V LMKN +V
Sbjct: 20	QPVRFDKVLYNQQGHYDPSTGKFTCPVPGVYYFSYHI-ESKGRNVKSLMKNGIQVMRE- 77
Query: 151	YDDGASRRREMQSOSVMLALRRGDAVWLLSHDHGYGAYSNHGKYITFSGFLVY 204
	D+ ++ S +L LR+GD VW L D G Y+ TFSGFL++
Sbjct: 78	CDEYQKGLYQVASGGALLQLRQGDQVW-LELDDKKNGLYAGEEVVDSTFSGFLLF 130 <u>(SEQ</u>
<u>ID NO: 182)</u>	

Table 3E Domain Analysis of NOV3

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain;
Phosphotransferases. Serine or threonine-specific kinase subfamily.

CD-Length = 256 residues, 100.0% aligned
Score = 237 bits (605), Expect = 1e-63

Query:	191	FSVHRIIGRGFGEVYGRKRDTGKMYAMKCLDKKRIKMKQGETLALNERIMLSLVSTGD
	250	+ + ++G+G FG+VY R + TGK+ A+K + K+++K K+ E L E +L + D
Subjct:	1	YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKRER-ILREIKILKLL--D
	56	
Query:	251	CPFIVCMSSYAFHTPDKLSFILDLMNGGDLHYHLSQHGVFSEADMRFYAAEIILGLEHMHN
	310	P IV + F DKL +++ GGDL L + G SE + RFYA +I+ LE++H+
Subjct:	57	HPNIVKLYDVFEDDDKLYLVMEYCEGGDLFDLLKKRGRRLSEDEARFYARQILSALEYLHS
	116	
Query:	311	RFVVYRDLKPANILLDEGHVRISDLGLACDFSKKKPHAS--VGTHGYMAPEVLQKGVAY
	368	+ +++RDLKP NILLD GHV++D GLA + VGT YMAPEVL G Y
Subjct:	117	QGIIHRDLKPENILLSDGHVKLADFGLAQLDSGGTLLTTFVGTPEYMAPEVL-LGKGY
	175	
Query:	369	DSSADWFSLGCMLFKLLRGHSPFRQHKTDK-HEIDRMTLTMAVELPDSFSPELHSILLEG
	427	+ D +SLG +L++LL G PF + SPE L++
Subjct:	176	GKAVIDWSLGVILYELLTGKPPPGDDQLLALFKKIGKPPPFPPPEWKISPEAKDLIKK
	235	
Query:	428	LLQRDVNRRLGCLGRGAQEVKESPFF 453
		LL +D +RL A+E E PFF
Subjct:	236	LLVKDPEKRL----TAAEALEHPFF 256 (SEQ ID NO: 183)

Table 3E on page 45 has been amended as follows:

The paragraph following Table 3E on page 45 has been amended as follows:

[gi|5139484|FKEACRLLRAPKFLNKPRSGTVELPKPSLCHPNSNGI]

Table 4E on page 63 has been amended as follows:

Table 4E. Domain Analysis of NOV4

gnl|Pfam|pfam01500, Keratin_B2, Keratin, high sulfur B2 protein. High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. This family has been divided up into four regions, with the second region containing 8 copies of a short repeat. This family is also known as B2 or KAP1.

CD-Length = 144 residues, 87.5% aligned

Score = 38.9 bits (89), Expect = 0.004

Query: 630	CIDVACSNHGTCITGTCICNPGYKGESCEEVDCMDPTCSGRGVCRGECHCFVGWGGTNC
689	C CS GTC + C + SC + C P CS C R C + C
Sbjct: 5	CGFPTCSTLGTGSSCC-----QPPSCCQPSCCQPVCQSQTCC-RPTCFQSSCCRPSCC
57	
Query: 690	ETP--RATCLDQCSCGHGTFLPDGLCSCDPSWTGHDCSIEIACAADC GG HG VCVGGT CRCE
747	+T + TC S G+ SC W DC +E
Sbjct: 58	QTSCCQPTCCQSSSCQ---TGCIGIGSCRTRWCRPDCRVE-----
93	
Query: 748	DGWMGAACDQRACHPRCAEHGTCRDGKCECS---PGWNGEHC 786
Sbjct: 94	-----GTCLPPCCVVSVSCTPPTCCQPVSAQASCCRPSYCGQSC 130 <u>(SEQ ID NO: 184)</u>

Table 6G on pages 84-85 has been amended as follows:

Table 6G. Domain Analysis of NOV6

gnl|Pfam|pfam01404, EPH_lbd, Ephrin receptor ligand binding domain. The Eph receptors, which bind to ephrins pfam00812 are a large family of receptor tyrosine kinases. This family represents the amino terminal domain which binds the ephrin ligand.

CD-Length = 174 residues, 100.0% aligned

Score = 345 bits (886), Expect = 6e-96

Query: 33	QVVLLDTSTVMGELGWKTYPLNGWDAITEMDEHNRPITHYQVCNVMEPNQNNWLRTNWIS	92
	+V LLDT+T GELGW TYP GW+ ++ +DE+NRPI TYQVCNVMEPNQNNWLRTNWIS	
Sbjct: 1	EVTLLDTTTATGELGWLTYPPGGWEEVSGLDENNRPIRTYQVCNVMEPNQNNWLRTNWIP	60

Query: 93	RDAAQKIQYVEMKFTLRCNSIPWVLGTCKETFTLYYIESDESHGTKFKPSQYIKIDTIAA	152
	R AQ++YVE+KFT+RDCNS+P VLGTCKETF LYy ESDE G ++ +QY K+DTIAA	
Sbjct: 61	RRGAQRVYVELKFTVRDCNSLPGVLGTCKETFNLYYYESDEDVGPRAWRENQYTKVDTIAA	120
Query: 153	DESFTQMDLGDRILKLNTIERVGPIERKGFYLAQFDIGACIALVSRVFYKKC	206
	DESFTQ+DLGDR++KLNT+E+R VGP+ +KGFYLAQFD+GAC+ALVSRVFYKKC	
Sbjct: 121 <u>ID NO: 185)</u>	DESFTQVDLGDRVMKLNTEVRSVGPLSKGFYLAQDVGACMALVSRVFYKKC	174 <u>(SEQ</u>

Table 7E on pages 92-93 has been amended as follows:

Table 7E. Domain Analysis of NOV7			
<u>gnl Pfam pfam00083, sugar_tr, Sugar (and other) transporter.</u>			
CD-Length = 447 residues, 96.6% aligned Score = 246 bits (629), Expect = 2e-66			
Query: 21	FQVFKSFYNETYFERHATFM---DGKLMLLLWSCTVSMFPLGGLLGSLLVGLLVDSCGR	76	
	V F F + +L VS+F +G +GSL G L D GR		
Sbjct: 16	TGVIGGFATLIDFLFFFGLTSSGSCAESTVLSGLVVSIFFVGRPIGSLFAGKLGDRFGR	75	
Query: 77	KGTLLINNIFAIIPAILMGVSKVAKAFELIVFSRVVLGVVCAGISYSALPMYLGEAPKNL	136	
	K +LLI + + I ++L G++ A F L++ RV++G+ G + +PMY+ E+APK L		
Sbjct: 76	KKSLLIGLVLFVIGSLLSGLAPGA--FYLLIVGRVLVGLGVGGASVLVPMYISEIAPKAL	133	
Query: 137	RGMVGTMTTEVFVIVGVFLAQIFSLQAILGNPAGWPVLLALTGVPAALLQLLTLPPFFPESPR	196	
	RG +G++ ++ + +G+ +A I L N GW + L L VPALL L+ L F PESPR		
Sbjct: 134	RGALGSLYQLGITIGLVAIIIGLGLNKTNNWGWRIPLGLQLVPALLLIGLLFLPESPR	193	
Query: 197	YSLIQKGDEATARPLRRLRGHTDMEAELEDMRAEARAERAEGHLSVLHLCALRSLRWQLL	256	
	+ +++ E L +LRG D++ E+++ +AE A + + R +LL		
Sbjct: 194	WLVLKGKLEEARAVLAKLRGVEDVDQEIQEEKAELEAGVSSEKAGLELF--RGRTRQRLL	251	
Query: 257	SIVVLMAQQQLSGINAINYYADTIYTSAGVEAAHSQYVTVGSGVVNIVMTITSVVLVERL	316	
	++L QQL+GINAI YY+ TI+ S G+ + + VT+ GVVN V T ++ LV+R		
Sbjct: 252	MGVMLQIFQQLTGINAIFYYSPTIFKSVGMSDSVALLVTIIVGVVNFVATFVAIFLVDRF	311	
Query: 317	GRRHLLLLAGYGICGSACLVLTVSPPPPQNRPPELSYLGIIICVFAYIAGHSIGPSPVPSVVR	376	
	GRR LLL G L+L V+ P + I+ + +IA ++G P+P V+		
Sbjct: 312	GRRPPLLGAAGMAICFLILGVA-LLLLNKPGAGIVVAIFILLFIAFFALGWGPIPWWIL	370	
Query: 377	TEIFLQSSRRAAFMVDGAVHWLTNFIIGFLFPSIQEAIQ-AYSFIIFAGICLLTAIYIYV	435	
	+E+F R A + A +WL NFIIGFLFP I AIG Y F+ FAG+ +L +++Y		
Sbjct: 371	SELFPTGVRSKAMALATAANWLANFIIGFLFPYITGAIGGGYVFLFFAGLLVLFILFVYF	430	
Query: 436	VIPETKGKTFVEINRIF 452		
	+PETKG+T EI+ +F		
Sbjct: 431	FVPETKGRTLEEIDEFL 447 <u>(SEQ ID NO: 186)</u>		

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Table 8E on page 101 has been amended as follows:

Table 8E. Domain Analysis of NOV8					
<u>gnl Smart smart00179</u> , EGF_CA, Calcium-binding EGF-like domain					
CD-Length = 41 residues, 80.5% aligned					
Score = 52.8 bits (125), Expect = 7e-08					
Query:	125	DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY	156		
		DIDEC C++GG CVNT GS+ C C GY			
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33	<u>(SEQ ID NO:</u>	
	<u>187)</u>				

Table 9E on page 109 has been amended as follows:

Table 9E. Domain Analysis of NOV9					
<u>gnl Smart smart00179</u> , EGF_CA, Calcium-binding EGF-like domain					
CD-Length = 41 residues, 80.5% aligned					
Score = 52.8 bits (125), Expect = 7e-08					
Query:	125	DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY	156		
		DIDEC C++GG CVNT GS+ C C GY			
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33	<u>(SEQ ID NO:</u>	
	<u>188)</u>				

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Table 10E on page 116 has been amended as follows:

Table 10G Domain Analysis of NOV10

gnl|Smart|smart00409, IG, Immunoglobulin

CD-Length = 86 residues, 89.5% aligned

Score = 37.0 bits (84), Expect = 0.001

Query: 27	SNVTLECNFDTGSHVNLDGAITVSLQKVENDTSPHRERATLLEEQLPLGKASFHI PQVQVR	86			
	+VTL C	TV+ K	R ++	G ++	I V
Sbjct: 10	ESVTLSCEASGNPPP-----	TVTWYKQGGKLLAESGRFSVSRSG---	GNSTLTISNVTP	E	61
Query: 87	DEGQYQCIIIIYGVAWDYKYLTLKV	111			
	D G Y C	TL V			
Sbjct: 62	DSGYTYTCAATNSSGSASSGTTLV	86 (SEQ ID NO: 189)			

Table 11E on page 123 has been amended as follows:

Table 11E. Domain Analysis of NOV11

gnl|Smart|smart00406, IgV, Immunoglobulin V-Type

CD-Length = 80 residues, 96.2% aligned

Score = 34.7 bits (78), Expect = 0.008

Query: 52	VELOCQLFPNISAEDMELRWYRCQPSLAVHMHERGMDMDGEQKWQYRGRTTFMSDHVARG	111
	V L C + + W R P + + Y+GR T D+ ++	
Sbjct: 2	VTLSCKASGF-TFSSYYVSWVRQPPGKGLELGYIGSDVSYS EASYKGRVTISKDN-SKN	59
Query: 112	KAMVRSHRVTTFDNRTYCC	130
	+ + D TY C	
Sbjct: 60	DVSLTISNLRVEDTGTYYC	78 (SEQ ID NO: 190)

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